

OIPE

RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/044,534

TIME: 09:06:46

```
1 <110> APPLICANT: Le, Junming
 2
         Vilcek, Jan
 3
         Daddona, Peter
                                                    ENTEREC
         Ghrayeb, John
         Knight, David M.
         Siegel, Scott
 6
   <120> TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
         Human Tumor Necrosis Factor
 9 <130> FILE REFERENCE: 0975.1005-013
10 <140> CURRENT APPLICATION NUMBER: 10/044,534
11 <141> CURRENT FILING DATE: 2002-01-10
13 <150> PRIOR APPLICATION NUMBER: 09/927,703
14 <151> PRIOR FILING DATE: 2001-08-10
16 <150> PRIOR APPLICATION NUMBER: U.S. 09/756,398
17 <151> PRIOR FILING DATE: 2001-01-08
18 <150> PRIOR APPLICATION NUMBER: U.S. 09/133,119
19 <151> PRIOR FILING DATE: 1998-08-12
20 <150> PRIOR APPLICATION NUMBER: U.S. 08/570,674
21 <151> PRIOR FILING DATE: 1995-12-11
22 <150> PRIOR APPLICATION NUMBER: U.S. 08/324,799
23 <151> PRIOR FILING DATE: 1994-10-18
24 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,102
25 <151> PRIOR FILING DATE: 1994-02-04
26 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,861
27 <151> PRIOR FILING DATE: 1994-02-04
28 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,093
29 <151> PRIOR FILING DATE: 1994-02-04
30 <150> PRIOR APPLICATION NUMBER: U.S. 08/010,406
31 <151> PRIOR FILING DATE: 1993-01-29
32 <150> PRIOR APPLICATION NUMBER: U.S. 08/013,413
33 <151> PRIOR FILING DATE: 1993-02-02
34 <150> PRIOR APPLICATION NUMBER: U.S. 07/943,852
35 <151> PRIOR FILING DATE: 1992-09-11
36 <150> PRIOR APPLICATION NUMBER: U.S. 07/853,606
37 <151> PRIOR FILING DATE: 1992-03-18
38 <150> PRIOR APPLICATION NUMBER: U.S. 07/670,827
39 <151> PRIOR FILING DATE: 1991-03-18
40 <160> NUMBER OF SEQ ID NOS: 19
41 <170> SOFTWARE: FastSEQ for Windows Version 4.0
43 <210> SEQ ID NO: 1
44 <211> LENGTH: 157
45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
```

RAW SEQUENCE LISTING DATE: 02/07/2002 PATENT APPLICATION: US/10/044,534 TIME: 09:06:46

```
47 <400> SEQUENCE: 1
 48
          Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
 49
 50
          Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 51
                                           25
 52
          Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
53
                                       40
54
          Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
55
56
          Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
57
          Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
58
59
                                               90
60
          Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
61
                                           105
62
          Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
63
                                       120
64
          Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
65
                                   135
          Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
66
67
                              150
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 321
71 <212> TYPE: DNA
72 <213> ORGANISM: Mus Balb/c
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1)...(321)
76 <400> SEQUENCE: 2
77
         gac atc ttg ctg act cag tct cca gcc atc ctg tct gtg agt cca gga
                                                                              48
78
         Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
79
          1
                           5
         gaa aga gtc agt ttc tcc tgc agg gcc agt cag ttc gtt ggc tca agc
80
                                                                              96
         Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
81
82
         atc cac tgg tat cag caa aga aca aat ggt tct cca agg ctt ctc ata
83
                                                                              144
         Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
84
85
                                       40
86
         aag tat get tet gag tet atg tet ggg ate eet tee agg tit agt gge
                                                                              192
         Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
87
88
              50
                                   55
89
         agt gga tca ggg aca gat ttt act ctt agc atc aac act gtg gag tct
                                                                              240
90
         Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
91
                                                    75
92
         gaa gat att gca gat tat tac tgt caa caa agt cat agc tgg cca ttc
                                                                              288
93
         Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
94
                           85
95
         acg ttc ggc tcg ggg aca aat ttg gaa gta aaa
                                                                             321
96
         Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
```



RAW SEQUENCE LISTING

DATE: 02/07/2002 TIME: 09:06:46

PATENT APPLICATION: US/10/044,534

99 < 210 > SEO ID NO: 3 100 < 211 > LENGTH: 107 101 < 212 > TYPE: PRT 102 < 213	97			1	.00				1	.05								
101 2212 TYPE: PRT 102 2213 ORGANISM: Mus Balb/c SEQUENCE: 3 104 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Is 15 106 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser 107 20 25 30 30 35 30 40 45 30 40 35 30 40 45 30 35 30 40 35 30 40 45 30 35 30 40 35 30 40 45 30 30 35 30 30 30 30 3		SEQ J	D NC): 3														
102	100 <211>	LENC	TH:	107														
103 400	101 <212>	TYPE	: PR	T														
105	102 <213>	ORG	NISM	i ։ Mu	ıs Ba	lb/c	2											
1	103 <400>	SEQU	JENCE	1: 3														
Single S	104	Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Val	Ser	Pro	Gly	
108	105					-												
11e His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile 109	106	Glu	Arg	Val	Ser	Phe	Ser	Cys	Arg	Ala	Ser	Gln	Phe	Val		Ser	Ser	
100	107																	
110	108	Ile	His	Trp	Tyr	Gln	Gln	Arg	Thr	Asn	Gly	Ser	Pro	Arg	Leu	Leu	Ile	
111	109																	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser	110	Lys	\mathtt{Tyr}	Ala	Ser	Glu	Ser	Met	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
113 65 70 75 80 114 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe 115 85 90 95 116 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys 117 100 105 119 <210> SEQ ID NO: 4 120 <211> LENGTH: 357 121 <212> TYPE: DNA 122 <213> ORGANISM: Mus Balb/c 123 <220> FEATURE: 124 <221> NAME/KEY: CDS 125 <222> LOCATION: (1)(357) 126 <400> SEQUENCE: 4 127 gaa gtg aag ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga ggc 128 Glu Val Lys Leu Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly 129 1 5 10 15 130 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac 96 131 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His 132 20 20 133 tgg atg aac tgg gtc cgc cag tct cca gag aag ggc ctt gag tgg gtt gre gag gg ctt gag gg ggc ttg gtg caa cac cac 96 131 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His 132 20 25 30 133 tgg atg aac tgg gtc cgc cag tct cca gag aag ggc ctt gag tgg gtt 144 134 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val 136 gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag 192 137 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu 138 50 50 50 50 50 60 140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 95 95 96 97 98 98 98 98 98 98 98 98 98	111															_		
114	112	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Ile	Asn	Thr	Val	Glu		
115	113															_		
116 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys 117 100 105 119 <210> SEQ ID NO: 4 120 <211> LENGTH: 357 121 <212> TYPE: DNA 122 <213> ORGANISM: Mus Balb/c 123 <220> FEATURE: 124 <221> NAME/KEY: CDS 125 <222> LOCATION: (1)(357) 126 <400> SEQUENCE: 4 127 gaa gtg aag ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga 128 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 129 1 5 10 130 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac 131 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His 132 20 25 30 133 tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gt 134 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val 135 35 40 45 136 gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag 137 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu 138 50 55 60 139 tct gtg aaa ggg agg ttc acc acc act tca aga gat gat tcc aaa agt gct 140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac agg tag acc tac tgg ggc caa 136 137 Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Typ Gly Gln	114	Glu	Asp	Ile	Ala	Asp	Tyr	Tyr	Cys	Gln		Ser	His	Ser	Trp		Phe	
117	115															95		
119 <210> SEQ ID NO: 4 120 <211> LENGTH: 357 121 <212> TYPE: DNA 122 <213> ORGANISM: Mus Balb/c 123 <220> FEATURE: 124 <221> NAME/KEY: CDS 125 <222> LOCATION: (1)(357) 126 <400> SEQUENCE: 4 127	116	Thr	Phe	Gly	Ser	Gly	Thr	Asn	Leu		Val	Lys						
120	117				100					105								
121	119 <210>	SEQ	ID N	10: 4	ļ													
122 <213> ORGANISM: Mus Balb/c 123 <220> FEATURE: 124 <221> NAME/KEY: CDS 125 <222> LOCATION: (1)(357) 126 <400> SEQUENCE: 4 127																		
123									. '									
124					ıs Ba	alb/d	2											
125 <222> LOCATION: (1)(357) 126 <400> SEQUENCE: 4 127																		
126																		
127					L)	. (35)	/)											
128											~~~	++~	~+ ~		aat	aas	aas	18
129		gaa	gtg	aag	CLL	gag	gag	Com	gga	gga	gge	LLY	y L y	Cln	Dro	Clu	gga Glw	40
130 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac 96 131 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His 132			Val	ьуs	Leu		GIU	ser	СТА	СТУ		ьeu.	vaı	GIII	FIU		GLY	
131							+ ~+	~++	aaa	+ 0+		++0	att	ttc	ant		cac	96
132 133 1 tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt 134 134 1 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val 135 136 137 138 139 140 150 150 150 150 150 150 150 150 150 15		TCC	atg	aaa	TOU	Cor	Cvc	yuu Wal	ycc λla	Cor	99a	Dho	Tla	Dhe	Ser	Asn	His	50
tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt 134		ser	мет	гуѕ		ser	Cys	vai	нта		СТУ	FIIE	116	FIIC		ASII	1115	
134 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val 135		+ ~ ~	2+4	220		at o	aaa	car	tot		αaα	aad	σσσ	ctt		tαα	at.t.	144
135		Tyy	Mot	Agn	Trn	Val	Ara	Cln	Ser	Dro	Glu	Lvg	Glv	T.eu	Glu	Tro	Val	
gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag 192 137 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu 138 50 55 60 139 tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct 140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac ggc tac tgg ggc caa 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln		ттр	Mec		тър	Val	мту	GIII		rio	Olu	כעם	0-1		024			
137 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu 138 50 55 60 139 tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct 140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln					aua	tca	aaa	tct		aat	tct	σса	aca		tat	aca	gag	192
138							uuu		466			500				712	21	
tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct 140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln		gct	Glu	Tle	Ara	Ser	Lvs	Ser	T1e	Asn	Ser	Ala	Thr	His	Tvr	Ата	GLU	
140 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala 141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 288 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 90 95 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137	Ala	Glu	Ile	Arg	Ser	Lys								Tyr	АІА	GIU	
141 65 70 75 80 142 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 288 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138	Ala	Glu 50	Ile	Arg	Ser	Lys	55					60					240
gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 143 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138 139	Ala	Glu 50 gtg	Ile aaa	Arg ggg	Ser agg	Lys ttc	55 acc	atc	tca	aga	gat	60 gat	tcc	aaa	agt	gct	240
Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138 139 140	Ala tct Ser	Glu 50 gtg	Ile aaa	Arg ggg	Ser agg	Lys ttc Phe	55 acc	atc	tca	aga	gat Asp	60 gat	tcc	aaa	agt	gct Ala	240
144 85 90 95 145 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336 146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138 139 140 141	Ala tct Ser 65	Glu 50 gtg Val	Ile aaa Lys	Arg ggg Gly	Ser agg Arg	Lys ttc Phe 70	55 acc Thr	atc Ile	tca Ser	aga Arg	gat Asp 75	60 gat Asp	tcc Ser	aaa Lys	agt Ser	gct Ala 80	
tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138 139 140 141 142	Ala tct Ser 65 gtc	Glu 50 gtg Val tac	Ile aaa Lys ctg	Arg ggg Gly caa	Ser agg Arg	ttc Phe 70 acc	55 acc Thr	atc Ile tta	tca Ser	aga Arg	gat Asp 75 gaa	60 gat Asp gac	tcc Ser	aaa Lys ggc	agt Ser gtt	gct Ala 80 tat	
146 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln	137 138 139 140 141 142 143	Ala tct Ser 65 gtc	Glu 50 gtg Val tac	Ile aaa Lys ctg	Arg ggg Gly caa	ser agg Arg atg Met	ttc Phe 70 acc	55 acc Thr	atc Ile tta	tca Ser	aga Arg act Thr	gat Asp 75 gaa	60 gat Asp gac	tcc Ser	aaa Lys ggc	agt Ser gtt Val	gct Ala 80 tat	
107	137 138 139 140 141 142 143	tct Ser 65 gtc Val	Glu 50 gtg Val tac Tyr	Ile aaa Lys ctg Leu	Arg ggg Gly caa Gln	ser agg Arg atg Met 85	ttc Phe 70 acc Thr	55 acc Thr gac Asp	atc Ile tta Leu	tca Ser aga Arg	aga Arg act Thr 90	gat Asp 75 gaa Glu	60 gat Asp gac Asp	tcc Ser act Thr	aaa Lys ggc Gly	agt Ser gtt Val 95	gct Ala 80 tat Tyr	288
	137 138 139 140 141 142 143 144	Ala tct Ser 65 gtc Val	Glu 50 gtg Val tac Tyr	Ile aaa Lys ctg Leu tcc	ggg Gly caa Gln	ser agg Arg atg Met 85 aat	ttc Phe 70 acc Thr	55 acc Thr gac Asp	atc Ile tta Leu	tca Ser aga Arg	aga Arg act Thr 90	gat Asp 75 gaa Glu tac	60 gat Asp gac Asp	tcc Ser act Thr	aaa Lys ggc Gly	agt Ser gtt Val 95 ggc	gct Ala 80 tat Tyr	288

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/044,534

DATE: 02/07/2002
TIME: 09:06:46

```
148
           ggc acc act ctc aca gtc tcc
                                                                               357
 149
           Gly Thr Thr Leu Thr Val Ser
 150
                   115
 152 <210> SEQ ID NO: 5
 153 <211> LENGTH: 119
 154 <212> TYPE: PRT
 155 <213> ORGANISM: Mus Balb/c
 156 <400> SEQUENCE: 5
           Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 157
 158
 159
           Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
 160
161
           Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
162
163
           Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
164
                                   55
165
          Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
166
                                                    75
167
          Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
168
                                                90
          Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
169
170
                       100
171
          Gly Thr Thr Leu Thr Val Ser
172
                   115
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 8
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 6
179
          Gly Thr Leu Val Thr Val Ser Ser
180
182 <210> SEQ ID NO: 7
183 <211> LENGTH: 7
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 7
187
          Gly Thr Lys Leu Glu Ile Lys
188
          1
190 <210> SEQ ID NO: 8
191 <211> LENGTH: 20
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: PCR oligonucleotides
196 <400> SEQUENCE: 8
197
         cctggatacc tgtgaaaaga
                                                                             20
199 <210> SEQ ID NO: 9
200 <211> LENGTH: 27
201 <212> TYPE: DNA
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/044,534

DATE: 02/07/2002 TIME: 09:06:46

202	2 <213	> ORGANISM: Artificial Sequence > FEATURE:	
204	· \4400	OTHER INFORMATION: PCR oligonucleotides SEQUENCE: 9	
	5		
		cctggtacct tagtcaccgt ctcctca SEQ ID NO: 10	27
		LENGTH: 27	
		TYPE: DNA	
211	. <2132	ORGANISM: Artificial Sequence	
		FEATURE:	
214	< 4.00	OTHER INFORMATION: PCR oligonucleotides	
		SEQUENCE: 10	
215		aatagatatc tccttcaaca cctgcaa	27
		SEQ ID NO: 11	
		LENGTH: 21	
219	<212>	TYPE: DNA	
220	· <213>	ORGANISM: Artificial Sequence	
		FEATURE:	
222	<223>	OTHER INFORMATION: PCR oligonucleotides	
223	<400>	SEQUENCE: 11	
		atcgggacaa agttggaaat a	21
226	<210>	SEQ ID NO: 12	21
		LENGTH: 16	
228	<212>	TYPE: DNA	
229	<213>	ORGANISM: Artificial Sequence	
230	<220>	FEATURE:	
231	<223>	OTHER INFORMATION: PCR oligonucleotides	
232	<400>	SEQUENCE: 12	
		ggcggtctgg taccgg	1.0
235	<210>	SEQ ID NO: 13	16
236	<211>	LENGTH: 19	
		TYPE: DNA	
238	<213>	ORGANISM: Artificial Sequence	
239	<220>	FEATURE:	
		OTHER INFORMATION: PCR oligonucleotides	
241	<400>	SEQUENCE: 13	
242		gtcaacaaca tagtcatca	
	<210>	SEQ ID NO: 14	19
245	<211>	LENGTH: 23	
		TYPE: DNA	
247	<213>	ORGANISM: Artificial Sequence	
248	<220>	FEATURE:	
250	<400	OTHER INFORMATION: PCR oligonucleotides SEQUENCE: 14	
251			
	/21A\	cacaggtgtg tccccaagga aaa	23
253	~~±U/ /211\	SEQ ID NO: 15 LENGTH: 18	
255	~&±±2 ~010×	TYPE: DNA	
2JJ 256	~&± <i>&</i> > ~919~	TIPE: UNA	
200	~ 213>	ORGANISM: Artificial Sequence	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/044,534

DATE: 02/07/2002 TIME: 09:06:47